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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=23; hr=13; min=45; sec=43; ms=375;]

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Reviewer Comments:

<120> A METHOD FOR CREATING A FUNCTIONALLY ACTIVE CHIMERIC TYPE IIG
RESTRICTION ENDONUCLEASE (as amended)

The first line of the above <120> response exceeds the Sequence Rules' required 72-character line (this includes white spaces). Please insert a hard return after "TYPE" on the first line, and align the second line.

(from Sequence 2)

Val	Asp	Glu	Ala	Leu	Leu	Ile	Lys	Tyr	His	Gly	Phe	Ser	Glu	Lys	Glu
				515						520					525

Val	Lys	Gln	Leu	Arg	Gly	Ile	Trp	Lys	Lys	Leu	Ser	Gln	Arg	Arg	Asn
				530						535					540

Asn Arg Thr Lys Lys
545

Please delete the excess blank lines above: only one blank line should separate each amino acid line.

<210> 38
<211> 103
<212> PRT
<213> artificial

<220>

<223> segment of protein sequence of catechol O-methyltransferase

<400> 39

Please change the above <210> response to "39." <210> 38 was already shown.

Application No: 10800946

Version No: 2.0

Input Set:**Output Set:****Started:** 2008-01-09 14:09:09.990**Finished:** 2008-01-09 14:09:12.054**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 64 ms**Total Warnings:** 25**Total Errors:** 2**No. of SeqIDs Defined:** 43**Actual SeqID Count:** 43

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)

Input Set:

Output Set:

Started: 2008-01-09 14:09:09.990
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 212	Invalid Sequence ID Number; Expected 39 as next SeqID but skipped
E 212	Invalid Sequence ID Number; Expected 39 as next SeqID but skipped

SEQUENCE LISTING

<110> Xu, Shuang-yong
Kobbe, Daniela
Zhu, Zhenyu
Samuelson, James

<120> A METHOD FOR CREATING A FUNCTIONALLY ACTIVE CHIMERIC TYPE IIG RESTRICTION ENDONUCLEASE
(as amended)

<130> NEB-183-CIP

<140> 10800946

<141> 2004-03-15

<150> 10/150,028

<151> 2002-05-17

<150> 09/693,146

<151> 2000-07-02

<160> 43

<170> PatentIn version 3.2 (1-26) and 3.4 (27-43)

<210> 1

<211> 1650

<212> DNA

<213> Bacillus pumilus

<220>

<221> CDS

<222> (1)..(1650)

<400> 1

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1 5 10 15	

tat tac acc cct aaa gtt att gct gac ttt tta tgt caa tgg agt att	96
Tyr Tyr Thr Pro Lys Val Ile Ala Asp Phe Leu Cys Gln Trp Ser Ile	
20 25 30	

caa gat gac aca aag agt gta ctt gaa ccc agt tgt gga gat ggt aat	144
Gln Asp Asp Thr Lys Ser Val Leu Glu Pro Ser Cys Gly Asp Gly Asn	
35 40 45	

ttt att gaa tcg gca ata ctt agg ttc aaa gaa ctt agt ata gat aat	192
Phe Ile Glu Ser Ala Ile Leu Arg Phe Lys Glu Leu Ser Ile Asp Asn	
50 55 60	

gaa caa ctt aaa gga aga att aca gga gta gag cta att gaa gaa gaa	240
Glu Gln Leu Lys Gly Arg Ile Thr Gly Val Glu Leu Ile Glu Glu Glu	
65 70 75 80	

gct ttg aaa gtt caa aat cga gca aat gag ttg ggg gtt gat aaa aac	288
Ala Leu Lys Val Gln Asn Arg Ala Asn Glu Leu Gly Val Asp Lys Asn	

tca ata gta aat agt gac ttc ttt caa ttt gta aaa gat aat aag aat	336
Ser Ile Val Asn Ser Asp Phe Phe Gln Phe Val Lys Asp Asn Lys Asn	
100 105 110	
aaa aaa ttt gat act att att ggt aat cca cca ttc ata aga tac caa	384
Lys Lys Phe Asp Thr Ile Ile Gly Asn Pro Pro Phe Ile Arg Tyr Gln	
115 120 125	
aac ttt cct gaa gag cat cgt agt ata gcc atg gaa atg atg gag gaa	432
Asn Phe Pro Glu Glu His Arg Ser Ile Ala Met Glu Met Met Glu Glu	
130 135 140	
cta ggt tta aaa cct aat aaa ctt aca aat atc tgg gtt cca ttt cta	480
Leu Gly Leu Lys Pro Asn Lys Leu Thr Asn Ile Trp Val Pro Phe Leu	
145 150 155 160	
gtg gta tct gct aca tta ctt aat gaa caa gga aag atg gct atg gtt	528
Val Val Ser Ala Thr Leu Leu Asn Glu Gln Gly Lys Met Ala Met Val	
165 170 175	
ata ccg gct gaa tta ttt cag gta aag tat gca gca gaa aca aga att	576
Ile Pro Ala Glu Leu Phe Gln Val Lys Tyr Ala Ala Glu Thr Arg Ile	
180 185 190	
ttt tta tca aag ttt ttc gat cgt atc act ata att aca ttt gaa aaa	624
Phe Leu Ser Lys Phe Phe Asp Arg Ile Thr Ile Ile Thr Phe Glu Lys	
195 200 205	
ctt gtt ttt gaa aat atc caa cag gaa gtt ata cta ctt ctt tgt gaa	672
Leu Val Phe Glu Asn Ile Gln Gln Glu Val Ile Leu Leu Leu Cys Glu	
210 215 220	
aag aaa gtt aat aaa ggt aaa gga att cgg gtt att gaa tgc gag aac	720
Lys Lys Val Asn Lys Gly Lys Gly Ile Arg Val Ile Glu Cys Glu Asn	
225 230 235 240	
tta gat gga tta aat tcc att gat ttt gta gct ata aat ggt tca aat	768
Leu Asp Gly Leu Asn Ser Ile Asp Phe Val Ala Ile Asn Gly Ser Asn	
245 250 255	
gtt aaa cct att gaa cac cgt act gaa aag tgg aca aag tat ttc tta	816
Val Lys Pro Ile Glu His Arg Thr Glu Lys Trp Thr Lys Tyr Phe Leu	
260 265 270	
aac gaa gat gaa ata ctt ctt tta cag agt tta aag gaa gac aaa cgc	864
Asn Glu Asp Glu Ile Leu Leu Leu Gln Ser Leu Lys Glu Asp Lys Arg	
275 280 285	
gtt aaa aat tgt aat gac tat ttt aag aca gaa gtt ggc tta gtt act	912
Val Lys Asn Cys Asn Asp Tyr Phe Lys Thr Glu Val Gly Leu Val Thr	
290 295 300	
gga cga aac gaa ttc ttt atg atg aaa gaa aac caa gta aaa gaa tgg	960
Gly Arg Asn Glu Phe Phe Met Met Lys Glu Asn Gln Val Lys Glu Trp	

305	310	315	320	
aat cta gaa gaa tat aca ata cct gtt aca ggt agg tcc aat cag tta Asn Leu Glu Glu Tyr Thr Ile Pro Val Thr Gly Arg Ser Asn Gln Leu				1008
	325	330	335	
aaa ggt ata aca ttt aca gaa aat gat ttt cat gaa aat tca atg gaa Lys Gly Ile Thr Phe Thr Glu Asn Asp Phe His Glu Asn Ser Met Glu				1056
	340	345	350	
caa aag gca att cac cta ttt ttg cca cca gat gaa gat ttt gaa aag Gln Lys Ala Ile His Leu Phe Leu Pro Pro Asp Glu Asp Phe Glu Lys				1104
	355	360	365	
tta ccg att gag tgt caa aat tat atc aag tat ggg gaa gaa aaa ggc Leu Pro Ile Glu Cys Gln Asn Tyr Ile Lys Tyr Gly Glu Glu Lys Gly				1152
	370	375	380	
ttc cat caa ggc tat aaa acc aga att aga aaa cgt tgg tat ata act Phe His Gln Gly Tyr Lys Thr Arg Ile Arg Lys Arg Trp Tyr Ile Thr				1200
	385	390	395	400
cca tct aga tgg gtt cca gat gct ttt gct tta aga cag gtt gat ggc Pro Ser Arg Trp Val Pro Asp Ala Phe Ala Leu Arg Gln Val Asp Gly				1248
	405	410	415	
tat cca aaa cta att tta aat gaa acc gac gct tct tct act gat aca Tyr Pro Lys Leu Ile Leu Asn Glu Thr Asp Ala Ser Ser Thr Asp Thr				1296
	420	425	430	
att cat agg gtt aga ttt aaa gaa ggt ata aat gaa aag tta gcc gta Ile His Arg Val Arg Phe Lys Glu Gly Ile Asn Glu Lys Leu Ala Val				1344
	435	440	445	
gtt tca ttt ttg aac tca ctc act ttt gca tct tca gaa ata acg ggg Val Ser Phe Leu Asn Ser Leu Thr Phe Ala Ser Ser Glu Ile Thr Gly				1392
	450	455	460	
aga agt tat ggt ggt ggt gtt atg aca ttc gaa cca act gaa att gga Arg Ser Tyr Gly Gly Gly Val Met Thr Phe Glu Pro Thr Glu Ile Gly				1440
	465	470	475	480
gaa atc cta ata cct tcc ttt gat aac tta tcc att gat ttt gat aaa Glu Ile Leu Ile Pro Ser Phe Asp Asn Leu Ser Ile Asp Phe Asp Lys				1488
	485	490	495	
att gat gcc tta att cga gaa aag gag att gaa aaa gtc ctt gat att Ile Asp Ala Leu Ile Arg Glu Lys Glu Ile Glu Lys Val Leu Asp Ile				1536
	500	505	510	
gtt gat gaa gct tta ctt ata aaa tat cat ggg ttt agt gag aaa gaa Val Asp Glu Ala Leu Leu Ile Lys Tyr His Gly Phe Ser Glu Lys Glu				1584
	515	520	525	
gta aaa cag ctt cga ggg ata tgg aag aaa ctt tct cag aga aga aac Val Lys Gln Leu Arg Gly Ile Trp Lys Lys Leu Ser Gln Arg Arg Asn				1632

530

535

540

aat aga acg aag aaa taa

1650

Asn Arg Thr Lys Lys

545 550

<210> 2

<211> 549

<212> PRT

<213> Bacillus pumilus

<400> 2

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1 5 10 15

Tyr Tyr Thr Pro Lys Val Ile Ala Asp Phe Leu Cys Gln Trp Ser Ile

20 25 30

Gln Asp Asp Thr Lys Ser Val Leu Glu Pro Ser Cys Gly Asp Gly Asn

35 40 45

Phe Ile Glu Ser Ala Ile Leu Arg Phe Lys Glu Leu Ser Ile Asp Asn

50 55 60

Glu Gln Leu Lys Gly Arg Ile Thr Gly Val Glu Leu Ile Glu Glu Glu

65 70 75 80

Ala Leu Lys Val Gln Asn Arg Ala Asn Glu Leu Gly Val Asp Lys Asn

85 90 95

Ser Ile Val Asn Ser Asp Phe Phe Gln Phe Val Lys Asp Asn Lys Asn

100 105 110

Lys Lys Phe Asp Thr Ile Ile Gly Asn Pro Pro Phe Ile Arg Tyr Gln

115 120 125

Asn Phe Pro Glu Glu His Arg Ser Ile Ala Met Glu Met Met Glu Glu

130 135 140

Leu Gly Leu Lys Pro Asn Lys Leu Thr Asn Ile Trp Val Pro Phe Leu

145 150 155 160

Val Val Ser Ala Thr Leu Leu Asn Glu Gln Gly Lys Met Ala Met Val

165 170 175

Ile Pro Ala Glu Leu Phe Gln Val Lys Tyr Ala Ala Glu Thr Arg Ile

180 185 190

Phe Leu Ser Lys Phe Phe Asp Arg Ile Thr Ile Ile Thr Phe Glu Lys

195 200 205

Leu Val Phe Glu Asn Ile Gln Gln Glu Val Ile Leu Leu Leu Cys Glu

210 215 220

Lys Lys Val Asn Lys Gly Lys Gly Ile Arg Val Ile Glu Cys Glu Asn

225		230		235		240
Leu Asp Gly	Leu Asn Ser Ile Asp Phe	Val Ala Ile Asn Gly	Ser Asn			
	245	250	255			
Val Lys Pro	Ile Glu His Arg Thr	Glu Lys Trp Thr	Lys Tyr Phe	Leu		
	260	265	270			
Asn Glu Asp	Glu Ile Leu Leu Leu Gln Ser	Leu Lys Glu Asp	Lys Arg			
	275	280	285			
Val Lys Asn	Cys Asn Asp Tyr Phe	Lys Thr Glu Val	Gly Leu Val	Thr		
	290	295	300			
Gly Arg Asn	Glu Phe Phe Met Met	Lys Glu Asn Gln	Val Lys Glu	Trp		
305	310	315	320			
Asn Leu Glu	Glu Tyr Thr Ile Pro	Val Thr Gly Arg	Ser Asn Gln	Leu		
	325	330	335			
Lys Gly Ile	Thr Phe Thr Glu Asn	Asp Phe His Glu	Asn Ser Met	Glu		
	340	345	350			
Gln Lys Ala	Ile His Leu Phe Leu	Pro Pro Asp Glu	Asp Phe Glu	Lys		
	355	360	365			
Leu Pro Ile	Glu Cys Gln Asn Tyr	Ile Lys Tyr Gly	Glu Glu Lys	Gly		
	370	375	380			
Phe His Gln	Gly Tyr Lys Thr Arg	Ile Arg Lys Arg	Trp Tyr Ile	Thr		
385	390	395	400			
Pro Ser Arg	Trp Val Pro Asp	Ala Phe Ala Leu	Arg Gln Val	Asp Gly		
	405	410	415			
Tyr Pro Lys	Leu Ile Leu Asn Glu	Thr Asp Ala Ser	Ser Thr Asp	Thr		
	420	425	430			
Ile His Arg	Val Arg Phe Lys Glu	Gly Ile Asn Glu	Lys Leu Ala	Val		
	435	440	445			
Val Ser Phe	Leu Asn Ser Leu Thr	Phe Ala Ser Ser	Glu Ile Thr	Gly		
	450	455	460			
Arg Ser Tyr	Gly Gly Gly Val Met	Thr Phe Glu Pro	Thr Glu Ile	Gly		
465	470	475	480			
Glu Ile Leu	Ile Pro Ser Phe Asp	Asn Leu Ser Ile	Asp Phe Asp	Lys		
	485	490	495			
Ile Asp Ala	Leu Ile Arg Glu Lys	Glu Ile Glu Lys	Val Leu Asp	Ile		
	500	505	510			
Val Asp Glu	Ala Leu Leu Ile Lys	Tyr His Gly Phe	Ser Glu Lys	Glu		
	515	520	525			

Val Lys Gln Leu Arg Gly Ile Trp Lys Lys Leu Ser Gln Arg Arg Asn
530 535 540

Asn Arg Thr Lys Lys
545

<210> 3

<211> 3030

<212> DNA

<213> Bacillus pumilus

<220>

<221> CDS

<222> (1)..(3030)

<400> 3

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1 5 10 15

ttt tta aaa cca act tat aat gaa act caa cta agg aat gat ttt ata 96
Phe Leu Lys Pro Thr Tyr Asn Glu Thr Gln Leu Arg Asn Asp Phe Ile
20 25 30

gac cca ctt cta aaa tct tta gga tgg gat gtt gat aat acc aaa gga 144
Asp Pro Leu Leu Lys Ser Leu Gly Trp Asp Val Asp Asn Thr Lys Gly
35 40 45

aaa aca cat att cta aga gat gtc att caa gaa gaa tac ata gaa ata 192
Lys Thr His Ile Leu Arg Asp Val Ile Gln Glu Glu Tyr Ile Glu Ile
50 55 60

aaa gat gag gag aca aag aaa aat cca gat tat aca ctt cgt ata aac 240
Lys Asp Glu Glu Thr Lys Lys Asn Pro Asp Tyr Thr Leu Arg Ile Asn
65 70 75 80

ggg acg aga aag ctg ttt gta gag gtt aag aaa ccg tct ttt aat att 288
Gly Thr Arg Lys Leu Phe Val Glu Val Lys Lys Pro Ser Phe Asn Ile
85 90 95

ttg aaa tca gct aaa gca gcc ttc caa aca aga aga tat ggt tgg agt 336
Leu Lys Ser Ala Lys Ala Ala Phe Gln Thr Arg Arg Tyr Gly Trp Ser
100 105 110

gct aac ctt ggt att tca gta ctt aca aat ttc gag cat cta gtt att 384
Ala Asn Leu Gly Ile Ser Val Leu Thr Asn Phe Glu His Leu Val Ile
115 120 125

tat gat tgt aga tat acg cct gac aaa tcc gac aat gaa cat att gct 432
Tyr Asp Cys Arg Tyr Thr Pro Asp Lys Ser Asp Asn Glu His Ile Ala
130 135 140

aga tat aaa gtt ttc tct tac gag gaa tat gaa gaa gca ttt gat gaa 480

Arg Tyr Lys Val Phe Ser Tyr Glu Glu Tyr Glu Glu Ala Phe Asp Glu	
145	150 155 160
ata aag gat ata att tca tat gag tca gcc aac tca ggt gct ctg gac	528
Ile Lys Asp Ile Ile Ser Tyr Glu Ser Ala Asn Ser Gly Ala Leu Asp	
165 170 175	
gaa atg ttt gat gta aat aca aga gtt ggt gaa acg ttt gac gag tat	576
Glu Met Phe Asp Val Asn Thr Arg Val Gly Glu Thr Phe Asp Glu Tyr	
180 185 190	
ttt tta cag caa att gag aat tgg cgc gaa aag cta gct aaa act gca	624
Phe Leu Gln Gln Ile Glu Asn Trp Arg Glu Lys Leu Ala Lys Thr Ala	
195 200 205	
att aaa aat aac acc gaa tta ggt gaa gag gac gtc aat ttt att gtc	672
Ile Lys Asn Asn Thr Glu Leu Gly Glu Glu Asp Val Asn Phe Ile Val	
210 215 220	
caa aga cta tta aac aga att att ttt ctt aga gtt tgt gaa gat aga	720
Gln Arg Leu Leu Asn Arg Ile Ile Phe Leu Arg Val Cys Glu Asp Arg	
225 230 235 240	
acc att gaa aaa tat gaa aca att aaa agt ata aaa aac tat gag gaa	768
Thr Ile Glu Lys Tyr Glu Thr Ile Lys Ser Ile Lys Asn Tyr Glu Glu	
245 250 255	
tta aaa gat ctg ttt caa aag tct gat agg aaa ttt aat tca ggt ctc	816
Leu Lys Asp Leu Phe Gln Lys Ser Asp Arg Lys Phe Asn Ser Gly Leu	
260 265 270	
ttt gac ttc ata gat gat acg ctc ttg ctt gag gtt gaa att gat tcg	864
Phe Asp Phe Ile Asp Asp Thr Leu Leu Leu Glu Val Glu Ile Asp Ser	
275 280 285	
aat gta ttg ata gaa att ttt agt gat tta tat ttc cca caa agc cca	912
Asn Val Leu Ile Glu Ile Phe Ser Asp Leu Tyr Phe Pro Gln Ser Pro	
290 295 300	
tat gat ttt tct gtt gtc gat cca aca ata tta agc cag ata tat gaa	960
Tyr Asp Phe Ser Val Val Asp Pro Thr Ile Leu Ser Gln Ile Tyr Glu	
305 310 315 320	
cgt ttt cta ggt caa gaa ata att ata gag tca ggt ggt aca ttt cac	1008
Arg Phe Leu Gly Gln Glu Ile Ile Ile Glu Ser Gly Gly Thr Phe His	
325 330 335	
att acg gag tca cca gaa gtt gcg gcg tcc aat ggt gtt gtt cca act	1056
Ile Thr Glu Ser Pro Glu Val Ala Ala Ser Asn Gly Val Val Pro Thr	
340 345 350	
cca aaa att atc gtc gaa cag ata gtg aaa gac act tta acg ccc ctt	1104
Pro Lys Ile Ile Val Glu Gln Ile Val Lys Asp Thr Leu Thr Pro Leu	
355 360 365	
acg gaa ggc aaa aaa ttt aat gag cta tgt aac tta aaa ata gca gat	1152
Thr Glu Gly Lys Lys Phe Asn Glu Leu Cys Asn Leu Lys Ile Ala Asp	

370

375

380

ata tgt tgt gga tca gga act ttc cta att tca agt tat gac ttt cta 1200
Ile Cys Cys Gly Ser Gly Thr Phe Leu Ile Ser Ser Tyr Asp Phe Leu
385 390 395 400

gta gag aaa gta atg gaa aag ata ata gaa gag aac atc gat gat tca 12